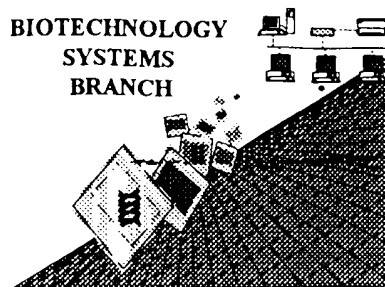


BIOTECHNOLOGY
SYSTEMS
BRANCH



#4
0500

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,756

Source: OIP

Date Processed by STIC: 10/4/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version of 37 CFR §§1.821 - 1.825 effective October 1, 1997 (new rules). The WIPO Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is 1.2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/670,756

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(NEW RULES) Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 12 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file resulting in misinterpretation of sequence identifiers and responses (as indicated in raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

P.6

RAW SEQUENCE LISTING
 PATENT APPLICATION N. US/09/670,756

DATE: 10/21/2001
 TIME: 10:17:51

Input File: A:\seqlist.txt
 Output File: N:\CRF3\10042000\I670756.raw

Does Not Comply
 Corrected Checklist Needed

1. 100- APPLICANT: BLANES, EUGENE
 2. 100- Betty, Maria
 3. 100- Linda, Maria-Pilar
 4. 100- An, Gueplan
 5. 100- TITLE OF INVENTION: CHANNEL INTERACT. PT AND USES THEREOF
 6. 100- FILE REFERENCE: HNT-0-001
 7. 100- CURRENT APPLICATION NUMBER: US/09/670,756
 8. 100- CURRENT FILING DATE: 2000-09-27
 9. 100- PRIOR APPLICATION NUMBER: USN 09/110,653
 10. 100- PRIOR FILING DATE: 1998-11-25
 11. 100- PRIOR APPLICATION NUMBER: USN 09/110,653
 12. 100- PRIOR FILING DATE: 1998-11-25
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RAW SEQUENCE LISTING

2014-07-12 20:01

PAPER: APPLICATION: US/09/670,756

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/670,756

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Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
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Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
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Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 65 70 75 80

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys (Xaa) Ile Tyr Ala Gln
 85 90 95

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
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Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 115 120 125

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
 130 135 140

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
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 165 170 175

Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
 180 185 190

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
 195 200

*See item 10
 on Error
 Summary
 sheet*

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

INPUT FILE: ALL N CS/09/670,756

DATE: 10/11/2010

TIME: 12:11:10

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Output Set: N:\CRF3\10042000\1670756.raw

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 L118 M:111 C: Current Filing Date differs. Replaced Current Filing Date
 L1282 M:111 W: (10) "n" or "Xaa" used; for SEQ ID# 11
 L1283 M:111 W: (10) "n" or "Xaa" used; for SEQ ID# 11
 L1284 M:111 W: Mandatory Feature missing. (20) not found for SEQ ID# 11
 L1285 M:128 W: Mandatory Feature missing. (21) not found for SEQ ID# 11
 L1286 M:128 W: Mandatory Feature missing. (21) not found for SEQ ID# 11
 L1287 M:128 W: Mandatory Feature missing. (21) not found for SEQ ID# 11
 L1288 M:128 W: Mandatory Feature missing. (21) not found for SEQ ID# 11
 L1289 M:141 W: (10) "n" or "Xaa" used; Feature required; for SEQ ID# 11
 L13028 M:141 W: (10) "n" or "Xaa" used; for SEQ ID# 13
 L13029 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 L13030 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 L13031 M:141 W: (10) "n" or "Xaa" used; Feature required; for SEQ ID# 13
 L13032 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 L13033 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 L13034 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 L13035 M:128 W: Mandatory Feature missing. (22) not found for SEQ ID# 13
 M:140 repeated in SeqID# 13